

SEARCH REQUEST FORM**Scientific and Technical Information Center**

Requester's Full Name: _____ Examiner # : _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.
 Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:	<u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #:	<u>124504</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location:		Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up:	<u>3/23</u>	Bibliographic _____	Dr.Link _____
Date Completed:	<u>3/24</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time:	<u>15</u>	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time:	<u>15</u>	Patent Family _____	WWW/Internet _____
Online Time:	<u>+15</u>	Other _____	Other (specify) _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 117502

TO: Phillip Gabel
Location: 3e81 / 3c70
Wednesday, March 24, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 955866

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

107502

Delaval, Jan

From: Gambel, Phillip
Sent: Tuesday, March 23, 2004 9:51 AM
To: Delaval, Jan
Subject: FW: roark amendment for new examiner 09/955,866

Subject: roark amendment for new examiner **09/955,866**

Jan

Please perform a sequence and a sequence interference search for

USSN 09 / 955,866 (roark amendment for new examiner)

- 1) SEQ ID NO: 1
- 2) SEQ ID NO: 1 as an "oligo"
- 3) SEQ ID NO: 2
- 4) SEQ ID NO: 2 as an "oligo"

Thanx

Phillip Gambel
Art Unit 1644
272-0844

1644 mailbox 3c70

RESULT 1
; Sequence 1, Application US/0955866
; Patent No. US2003010763A1
; GENERAL INFORMATION:
; APPLICANT: FOX, Michael

; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00-759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIORITY APPLICATION NUMBER: 60/233,867
; PRIORITY FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (33). (854)
; NAME/KEY: sig peptide
; LOCATION: (33). (89)
; NAME/KEY: msc feature
; LOCATION: (693). (755)
; OTHER INFORMATION: predicted transmembrane domain
; US-09-955-866-1

Query Match 100.0%; Score 1209; DB 9; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	DB	QY	DB
1	1	CAGAAAGGACCTATATGATCAAATAAGAAAGATGATTTCTCTCTGTAATGTTGAGCC	60
		CAGAAAGGACCTATATGATCAAATAAGAAAGATGATTTCTCTCTGTAATGTTGAGCC	60
61	61	TGGATTGAGCTTCACCATGAGCTTATTACAGTGACAGCCTAGGAATGT	120
		TGGATTGAGCTTCACCATGAGCTTATTACAGTGACAGCCTAGGAATGT	120
121	121	ACATAATAGCATGGCGAACATGCAATTGAACTTGAACACTGAACTCATG	180
		ACATAATAGCATGGCGAACATGCAATTGAACTTGAACACTGAACTCATG	180
121	121	ATCATATAGCATGGCGAACATGCAATTGAACTTGAACACTGAACTCATG	180
		ATCATATAGCATGGCGAACATGCAATTGAACTTGAACACTGAACTCATG	180
181	181	TGAACCTTGGAGAAATAACGCCATTGCAAAAGETGGAAATGATACATCCCACCC	240
		TGAACCTTGGAGAAATAACGCCATTGCAAAAGETGGAAATGATACATCCCACCC	240
181	181	ACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC	240
		ACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC	240
241	241	GTCAAAGGCCACTTGTGGAGGAGGCCCTTAGGGAGGCCCTGTTCCACATAC	300
		GTCAAAGGCCACTTGTGGAGGAGGCCCTTAGGGAGGCCCTGTTCCACATAC	300
241	241	GTCAAAGGCCACTTGTGGAGGAGGCCCTTAGGGAGGCCCTGTTCCACATAC	300
		GTCAAAGGCCACTTGTGGAGGAGGCCCTTAGGGAGGCCCTGTTCCACATAC	300
301	301	CTCAGTCCAATGTTGAGGAGAACCTGATGTTGATGGGGTGCCT	360
		CTCAGTCCAATGTTGAGGAGAACCTGATGTTGATGGGGTGCCT	360
301	301	CTCAGTCCAATGTTGAGGAGAACCTGATGTTGATGGGGTGCCT	360
		CTCAGTCCAATGTTGAGGAGAACCTGATGTTGATGGGGTGCCT	360
421	421	TCTTAAGTTCCAGAACAGTGGTAGACTCAGCTGCOAGGTACAGTTATCTC	480
		TCTTAAGTTCCAGAACAGTGGTAGACTCAGCTGCOAGGTACAGTTATCTC	480
421	421	TCTTAAGTTCCAGAACAGTGGTAGACTCAGCTGCOAGGTACAGTTATCTC	480
		TCTTAAGTTCCAGAACAGTGGTAGACTCAGCTGCOAGGTACAGTTATCTC	480
481	481	TGGAAAGACTATCTGGCCAAAGTCACGTTCTGGCCAAACCCAGCACTCGAGCCC	540
		TGGAAAGACTATCTGGCCAAAGTCACGTTCTGGCCAAACCCAGCACTCGAGCCC	540
541	541	CTGAAAGGCCCTCACAGGTCACAGGTCACAGGTCACAGGTCACAGGTCACAGG	600
		CTGAAAGGCCCTCACAGGTCACAGGTCACAGGTCACAGGTCACAGGTCACAGG	600
601	601	TCACTGTTGTTCTGGAACTACTCAGTGGCTAAAGCCACCCCTGGGAGAACT	660
		TCACTGTTGTTCTGGAACTACTCAGTGGCTAAAGCCACCCCTGGGAGAACT	660
601	601	TCACTGTTGTTCTGGAACTACTCAGTGGCTAAAGCCACCCCTGGGAGAACT	660

ALIGNMENTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 01:43:25 ; Search time 462 Seconds
(without alignments)

Title: US-09-955-866-1
Perfect score: 1209
Sequence: 1 cagaatagacccatatgtatgat.....agtttctaaatgtattcca 1209

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Gapop_60.0 , Gapext 60.0

Searched: 2438257 seqs, 1849576744 residues

Word size : 0

Total number of hits satisfying chosen parameters:

4876514

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 150 summaries

Database : Published Applications NA: *

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3: /cgns_6/_prodatal2/_pubpna/_US06_PUBCOMB.seq: *
4: /cgns_6/_prodatal2/_pubpna/_US06_PUBCOMB.seq: *
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7: /cgns_6/_prodatal2/_pubpna/_US08_PUB.seq: *
8: /cgns_6/_prodatal2/_pubpna/_US08_PUBCOMB.seq: *
9: /cgns_6/_prodatal2/_pubpna/_US09A_PUBCOMB.seq: *
10: /cgns_6/_prodatal2/_pubpna/_US09B_PUBCOMB.seq: *
11: /cgns_6/_prodatal2/_pubpna/_US09C_PUBCOMB.seq: *
12: /cgns_6/_prodatal2/_pubpna/_US09_NEW_PUB.seq: *
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17: /cgns_6/_prodatal2/_pubpna/_US60_NEW_PUB.seq: *
18: /cgns_6/_prodatal2/_pubpna/_US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	120.9	100.0	120.9	US-09-955-866-1
2	119.1	98.5	222.9	US-09-910-174A-20
3	119.1	98.5	224.2	US-09-814-353-21297
4	119.1	98.5	23.5	US-09-815-338-14
5	119.1	98.5	243.5	US-10-077-033-14
6	115.5	95.5	220.0	US-10-120-988-309
7	114.0	94.3	238.6	US-10-041-319-4
8	96.4	79.7	122.3	US-09-893-837-1
9	96.4	79.7	122.3	US-09-896-912A-1
10	89.1	79.7	122.3	US-10-034-650-41
11	73.7	240.6	15	US-10-023-333-3
12	82.3	68.1	84.2	US-09-875-338-20
13	82.3	68.1	84.2	US-10-077-023-20
14	82.2	68.0	82.2	US-10-041-319-5
15	82.2	68.0	82.2	US-10-034-650-42

Result No.	Score	Query Match Length	DB ID	Description
1	120.9	100.0	120.9	US-09-955-866-1
2	119.1	98.5	222.9	US-09-910-174A-20
3	119.1	98.5	224.2	US-09-814-353-21297
4	119.1	98.5	23.5	US-09-815-338-14
5	119.1	98.5	243.5	US-10-077-033-14
6	115.5	95.5	220.0	US-10-120-988-309
7	114.0	94.3	238.6	US-10-041-319-4
8	96.4	79.7	122.3	US-09-893-837-1
9	96.4	79.7	122.3	US-09-896-912A-1
10	89.1	79.7	122.3	US-10-034-650-41
11	73.7	240.6	15	US-10-023-333-3
12	82.3	68.1	84.2	US-09-875-338-20
13	82.3	68.1	84.2	US-10-077-023-20
14	82.2	68.0	82.2	US-10-041-319-5
15	82.2	68.0	82.2	US-10-034-650-42

Sequence 1, Appli

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Sequence 155, Appli

Sequence 156, Appli

Sequence 157, Appli

Sequence 158, Appli

Sequence 159, Appli

Sequence 15964, A

Sequence 15977, A

ATTACHMENTS

RESULT 1
AAD36968 standard; DNA; 1209 BP.
AAD36968;
Human B7-Like (B7-L) gene.
Human; B7-L protein; cell proliferation; arteriosclerosis; cancer; vascular restenosis; infertility; miscarriage; pre-term labour; delivery; endometriosis; T-cell function; psoriasis; autoimmune disease; systemic lupus erythematosus; antiinflammatory;
21-AUG-2002 (first entry)
Human B7-like (B7-L) gene.
Query Match 100.0%; Score 1209; DB 6; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 1209 BP; 354 A; 325 C; 250 G; 280 T; 0 U; 0 Other;
SQ CAGAAAGACCTATATGATCAAATACAGAACATGATCTCCCTGCTTAATGTGAGCC 60
QY CAGAAAGACCTATATGATCAAATACAGAACATGATCTCCCTGCTTAATGTGAGCC 60
DB CAGAAAGACCTATATGATCAAATACAGAACATGATCTCCCTGCTTAATGTGAGCC 60
61 TGGAAATTCAGCTTCAACAGATAGCAGCTTATTCACTACAGTACAGCTTCTAAGGA 120
61 TGGAAATTCAGCTTCAACAGATAGCAGCTTATTCACTACAGTACAGCTTCTAAGGA 120

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 22:59:39 : Search time 516 Seconds

(without alignments)

9953.627 Million cell updates/sec
 1 cagaatagacatattatgtat.....agtttctaaqtgatttcca 1209

Title: US-09-955-866-1

Scoring table: OLIGO_NUC

GapOp_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters:

6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqm2000s:*

4: Geneseqm2001as:*

5: Geneseqm2001bs:*

6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

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Post-processing: Listing first 150 summaries

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8: Geneseqm2003bs:*

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10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

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6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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2: Geneseqn1990s:*

3: Geneseqm2000s:*

4: Geneseqm2001as:*

5: Geneseqm2001bs:*

6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqm2000s:*

4: Geneseqm2001as:*

5: Geneseqm2001bs:*

6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

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10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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2: Geneseqn1990s:*

3: Geneseqm2000s:*

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5: Geneseqm2001bs:*

6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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7: Geneseqm2003as:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqm2000s:*

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7: Geneseqm2003as:*

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Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqm2000s:*

4: Geneseqm2001as:*

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6: Geneseqm2002s:*

7: Geneseqm2003as:*

8: Geneseqm2003bs:*

9: Geneseqm2003cs:*

10: Geneseqm2004s:*

Post-processing: Listing first 150 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3:

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! nucleic - nucleic search, using sw model

	on:	March 24, 2004, 00:06:30 ; Search time 2997 Seconds (without alignments) 12046.505 Million cell updates/sec
title:	US-09-955-866-1	
perfect score:	1209	
sequence:	1 cagaagagacccatatatgt.....agttttaaagtatttcac 1209	
scoring table:	OLIGO NUC	
gapop:	Gapext 60.0 , Gapext 60.0	
searched:	27513289 seqid, 14931090276 residues	
word size :	0	
total number of hits satisfying chosen parameters:	55026578	
minimum DB seq length:	0	
maximum DB seq length:	2000000000	
st-processing: Listing first 150 summaries		
database :	EST:*	
	1: em_estba:*	
	2: em_esthum:*	
	3: em_estin:*	
	4: em_estmu:*	
	5: em_estov:*	
	6: em_estpl:*	
	7: em_estro:*	
	8: em_htc:*	
	9: gb_est1:*	
	10: gb_est2:*	
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	26: em_gss_pbg:*	
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	29: gb_gssbt2:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult	No.	Query Score	Match Length	DB ID	Description
	1	635	52.5	906	14 CA483316
	2	558	46.2	793	9 AU135508
	3	292	24.2	534	12 BI001901
	4	20.6	579	10 AW961323	AW961323 ESM373395

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. This is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	DB	ID	Description	
1	635	52.5	906	14	CA449316	CA449316 AGENRCOURT	
2	558	46.2	793	9	AU133908	AU135908 AU135908	
C	3	292	24.2	534	12	BIO1901	BIO1901 PMO-THN007
C	4	249	20.6	579	10	AW961323	AW961323 EST3-THN395

101	1.3	1152	4	US-09-312-283C-42	Appl	Sequence 42, Appl	Length: 2229
102	1.3	1152	4	US-09-312-283C-211	Appl	Sequence 211, Appl	TYPE: DNA
103	1.3	1275	4	US-09-107-532A-2687	Appl	Sequence 2887, Appl	ORGANISM: Homo sapiens
104	1.3	1341	4	US-09-177-650-129	Appl	Sequence 129, Appl	FEATURE:
105	1.3	1401	4	US-09-489-039A-6779	Appl	Sequence 6779, Appl	NAME/KEY: misc_feature
106	1.3	1467	4	US-09-252-911A-7745	Appl	Sequence 7745, Appl	LOCATION: (1) . . . (2229)
107	1.3	1488	4	US-09-252-911A-7658	Appl	Sequence 7658, Appl	OTHER INFORMATION: n = A,T,C or G
108	1.3	1333	4	US-09-934-903-15	Appl	Sequence 15, Appl	FEATURE:
109	1.3	1746	4	US-09-107-532A-3181	Appl	Sequence 3181, Appl	NAME/KEY: CDS
110	1.3	1902	4	US-09-489-039A-7148	Appl	Sequence 7148, Appl	LOCATION: (78) . . . (896)
111	1.3	2198	4	US-09-205-258-112	Appl	Sequence 112, Appl	FEATURE:
112	1.3	2199	1	US-08-144-602B-5	Appl	Sequence 5, Appl	NAME/KEY: misc_feature
113	1.3	2346	4	US-09-484-970B-56	Appl	Sequence 56, Appl	LOCATION: (1) . . . (2229)
114	1.3	2346	4	US-09-484-970B-56	Appl	Sequence 56, Appl	OTHER INFORMATION: B7-H2 Long
115	1.3	2432	3	US-08-974-022-1	Appl	Sequence 1, Appl	US-09-910-174B-1
116	1.3	2432	3	US-08-795-445A-1	Appl	Sequence 1, Appl	
117	1.3	2432	3	US-08-795-447A-1	Appl	Sequence 1, Appl	
118	1.3	2432	3	US-08-974-186-1	Appl	Sequence 1, Appl	
119	1.3	2432	3	US-08-795-446B-1	Appl	Sequence 1, Appl	
120	1.3	2432	4	US-08-706-945D-123	Appl	Sequence 123, Appl	
121	1.3	2432	4	US-08-780-780-1	Appl	Sequence 1, Appl	
122	1.3	2434	4	US-09-665-720A-3	Appl	Sequence 3, Appl	
123	1.3	2434	4	US-09-665-720A-3	Appl	Sequence 5, Appl	
124	1.3	2475	3	US-09-232-658-5	Appl	Sequence 5, Appl	
125	1.3	2539	3	US-09-749-522-3	Appl	Sequence 3, Appl	
126	1.3	2625	3	US-08-804-439A-7	Appl	Sequence 7, Appl	
127	1.3	2625	3	US-08-720-229-7	Appl	Sequence 7, Appl	
128	1.3	2632	3	US-0-258-287B-51	Appl	Sequence 51, Appl	
129	1.3	2659	3	US-08-749-522-1	Appl	Sequence 1, Appl	
130	1.3	2914	4	US-09-177-650-6	Appl	Sequence 1, Appl	
131	1.3	2993	2	US-08-415-593-42	Appl	Sequence 6, Appl	
132	1.3	3051	4	US-09-409-604-20	Appl	Sequence 4, Appl	
133	1.3	3186	1	US-08-721-258-8	Appl	Sequence 1, Appl	
134	1.3	3186	2	US-08-977-306-8	Appl	Sequence 6, Appl	
135	1.3	3186	2	US-08-977-306-8	Appl	Sequence 8, Appl	
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138	1.3	3528	4	US-09-219-865B-1	Appl	Sequence 9, Appl	
139	1.3	3702	4	US-09-318-352-3748	Appl	Sequence 14, Appl	
140	1.3	3721	4	US-09-620-312D-300	Appl	Sequence 1, Appl	
141	1.3	3748	2	US-08-938-240-1	Appl	Sequence 1, Appl	
142	1.3	3900	4	US-09-984-970B-27	Appl	Sequence 27, Appl	
143	1.3	4406	1	US-08-369-043-1	Appl	Sequence 1, Appl	
144	1.3	4550	3	US-09-38-907-182	Appl	Sequence 182, Appl	
145	1.3	4550	4	US-09-218-207-182	Appl	Sequence 182, Appl	
146	1.3	4849	4	US-09-620-312D-39	Appl	Sequence 39, Appl	
147	1.3	5214	4	US-09-546-312D-32	Appl	Sequence 2, Appl	
148	1.3	5643	1	US-08-144-602B-4	Appl	Sequence 4, Appl	
149	1.3	6337	4	US-09-320-312D-1063	Appl	Sequence 1063, Appl	
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						QY	559 TCACCAAGCTTCCTCGCCCTAAAGCCACCCCCCTGGCAAAACTCTAGCTGTGTCTGG 618
						Db	604 TCACCAAGCTTCCTCGCCCTAAAGCCACCCCCCTGGCAAAACTCTAGCTGTGTCTGG 663
						QY	619 ATACTAAGTGGAGGAATTCTAGCCGAACTTGTGCAATTTGGCCAGATGGAACTCTG 738
						APPLICANT: Coyle, Anthony J.	CURRENT APPLICATION NUMBER: US/09/910,174B
						APPLICANT: Fraser, Christopher C.	PATENT NO. 6630575
						APPLICANT: Manning, Stephen	TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
						FILE REFERENCE: 35800/236924	FILE NUMBER: US/09/910,174B
						CURRENT APPLICATION NUMBER: US/09/910,174B	PATENT FILING DATE: 2001-07-20
						PRIOR APPLICATION NUMBER: US/09/620,461	PRIOR FILING DATE: 2000-07-20
						SEQ ID NOS: 32	SOFTWARE: fastSEQ for Windows Version 4.0
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9	330	27.3	401	4	US-09-643-597-264	
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12	330	27.3	401	4	US-09-606-421B-264	
13	35	2.9	744	4	US-09-910-174B-30	
14	21	1.7	38	4	US-09-910-174B-25	
15	21	1.7	38	4	US-09-620-161-25	
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17	20	1.7	477	4	US-09-519-332-49	
18	19	1.6	75395	4	US-09-620-461-26	
19	18	1.5	2160	4	US-09-716-129-12	
20	17	1.4	379	4	US-09-621-976-13874	
21	17	1.4	466	4	US-09-621-976-1443	
22	17	1.4	491	4	US-09-621-976-17688	
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24	17	1.4	498	4	US-09-519-232-47	
25	17	1.4	591	2	US-08-704-473-1	
26	17	1.4	594	3	US-09-188-930-42	
27	17	1.4	594	3	US-09-188-930-211	
28	17	1.4	597	4	US-09-489-139A-2817	
C	28	17	1.4	612	3	Sequence 400, App
C	30	17	1.4	744	4	Sequence 11267, A
C	31	17	1.4	918	4	Sequence 223, App
C	32	17	1.4	1105	4	Sequence 17, Appl
C	33	17	1.4	1105	4	Sequence 17, Appl
C	34	17	1.4	1105	4	Sequence 17, Appl
C	35	17	1.4	1105	4	Sequence 17, Appl
C	36	17	1.4	1108	2	Sequence 2, Appl
C	37	17	1.4	1194	4	Sequence 495, App
C	38	17	1.4	1485	4	Sequence 3069, App
C	39	17	1.4	2635	4	Sequence 121, App
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C	41	17	1.4	2768	1	Sequence 1, Appl
C	42	17	1.4	2768	1	Sequence 1, Appl
C	43	17	1.4	4926	2	Sequence 1, Appl
C	44	17	1.4	5080	4	Sequence 495, App
C	45	17	1.4	5824	4	Sequence 72, Appl
C	46	17	1.4	5924	4	Sequence 130, App
C	47	17	1.4	13674	2	Sequence 1, Appl
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C	75	16	1.3	593	4	Sequence 7, Appl
C	76	16	1.3	606	4	Sequence 2722, App
C	77	16	1.3	684	4	Sequence 1441, App
C	78	16	1.3	684	4	Sequence 1441, App
C	79	16	1.3	684	4	Sequence 1441, App
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C	81	16	1.3	717	4	Sequence 1908, App
C	82	16	1.3	726	4	Sequence 23, Appl
C	83	16	1.3	726	4	Sequence 24, Appl
C	84	16	1.3	889	4	Sequence 143, App
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C	86	16	1.3	730	4	Sequence 143, App
C	87	16	1.3	915	4	Sequence 143, App
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C	90	16	1.3	889	4	Sequence 1190, App
C	91	16	1.3	909	4	Sequence 5113, App
C	92	16	1.3	920	4	Sequence 3290, App
C	93	16	1.3	954	4	Sequence 19, App
C	94	16	1.3	954	4	Sequence 1428, App
C	95	16	1.3	1001	4	Sequence 45, App
C	96	16	1.3	1006	4	Sequence 386, App
C	97	16	1.3	1059	4	Sequence 115, App
C	98	16	1.3	1059	4	Sequence 42, App
C	99	16	1.3	1152	3	Sequence 211, App

2.1 25 AX411802 Sequence 139 20 1..7 159770 2 BX571700 Danio rerio
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 2.1 34 AX58043 Sequence C 141 20 1..7 163996 9 AC104384 Homo sapi
 2.0 31 AX58045 Sequence C 142 20 1..7 164882 8 AC123520 Oryza sativa
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 2.0 2 AC01323 Mus musculus C 144 20 1..7 171713 2 AL356152 Homo sapi
 2.0 266651 10 AC130711 Mus musculus C 145 20 1..7 172126 8 AC116368 Oryza sativa
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 2.0 20 1..7 153264 2 AC135216 Human DNA C 200 20 1..7 174554 2 AC120269 Rattus norvegicus

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 00:02:04 ; Search time 4686 Seconds

11182.614 Million cell updates/sec
 (without alignments)

Title: US-09-955-866-1

Perfect score: 1209

Sequence: 1 cagaaggacattatgtat.....agtttctaaatgttccaa 1209

Scoring table: Oligo_NUC

Gapext 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 150 summaries

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16: em_fur:*

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19: em_mu:*

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21: em_or:*

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em_ro:*

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em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	
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5	1191	98.5	2229	6 AX370286	Sequence	
6	1191	98.5	2435	6 AX357968	Sequence	
7	1140	94.3	2386	6 AX698331	Sequence	
8	954	79.7	1223	6 AX420002	Sequence	
9	964	79.7	1223	6 AX460797	Sequence	
10	964	79.7	1223	6 AX695966	Sequence	
11	964	79.7	1223	9 AF344424	Homo sapi	
12	823	68.1	842	6 AX357974	Sequence	
13	822	68.0	822	6 AX695967	Sequence	
14	822	68.0	822	6 AX698932	Sequence	
15	822	68.0	822	6 AY251343	Homo sapi	
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17	819	67.7	819	6 AR411239	Sequence	
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20	819	67.7	819	6 AX420004	Sequence	
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22	819	67.7	819	6 BD161902	Novel den	
23	779	64.4	1819	6 AX877717	Sequence	
24	779	64.4	1819	9 AK001872	Primer to	
25	779	64.4	1819	6 BD156810	Human DNA	
26	600	49.6	1356	6 AX357970	Sequence	
27	558	46.2	793	6 AX869415	Sequence	
28	558	46.2	793	6 BD19477	Primer to	
29	546	45.2	1975	6 AR407782	Sequence	
30	546	45.2	1975	6 AR411238	Sequence	
31	546	45.2	1975	6 AX370288	Sequence	
32	361	29.9	549	6 AR407784	Sequence	
33	361	29.9	549	6 AR411240	Sequence	
34	361	29.9	549	6 AX370306	Sequence	
35	361	29.9	19217	6 AX411791	Sequence	
36	361	29.9	79684	6 AX695965	Sequence	
37	361	29.9	146327	9 AL162253	Human DNA	
38	330	27.3	401	6 BD275827	COMPOUNDS	
39	330	27.3	401	6 AR2200612	Sequence	
40	330	27.3	401	6 AR255606	Sequence	
41	330	27.3	401	6 AR281176	Sequence	
42	330	27.3	401	6 AX365871	Sequence	
43	324	26.8	660	6 AX556518	Sequence	
44	309	25.6	9179	6 AX411789	Sequence	
45	304	25.1	861	6 AX556516	Sequence	
46	274	22.7	1814	6 AX411790	Sequence	
c	47	70	5.8	7979	6 AX403681	Homo sapi
c	48	70	5.8	1799	6 AX411787	Sequence
c	49	45	3.7	245032	2 AC096309	Rattus no
c	50	45	3.7	261001	2 AC096324	Rattus no
c	51	35	2.9	2741	6 AX420007	Sequence
c	52	35	2.9	741	6 AX460802	Sequence
c	53	35	2.9	744	6 AR407790	Sequence
c	54	35	2.9	744	6 AX354741	Sequence
c	55	35	2.9	744	6 AX370315	Sequence
c	56	35	2.9	744	6 AX695963	Sequence
c	57	35	2.9	744	6 AX95964	Sequence
c	58	35	2.9	1655	6 AX354739	Sequence
c	59	35	2.9	1655	6 AX420005	Sequence
c	60	35	2.9	1655	6 AX460800	Sequence
c	61	35	2.9	1655	10 AF147780	Mus muscu
c	62	35	2.9	7808	6 AX695962	Sequence
c	63	35	2.9	308333	6 AC093339	Mus muscu
c	64	27	2.2	27	6 AX411799	Sequence
c	65	26	2.2	26	6 AX411803	Sequence